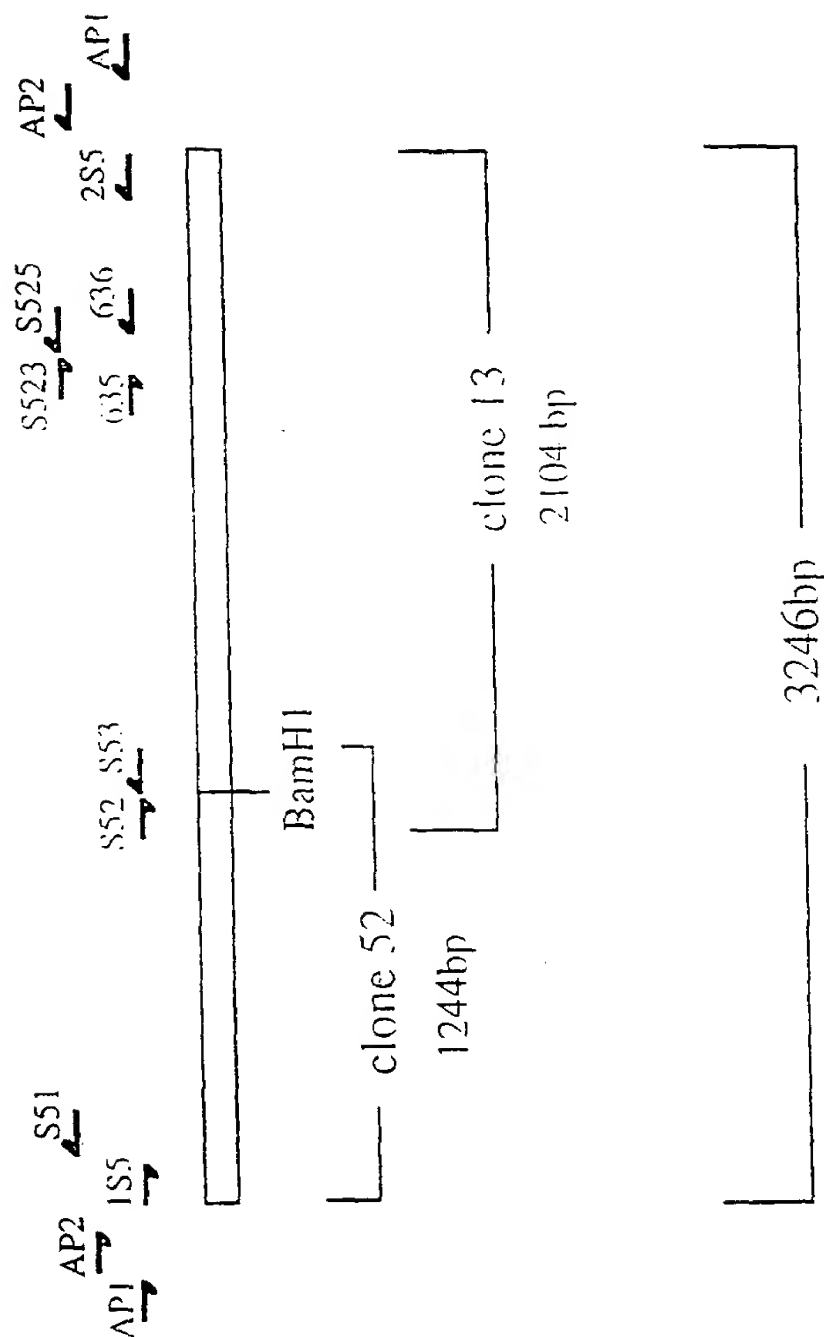


Figure 1



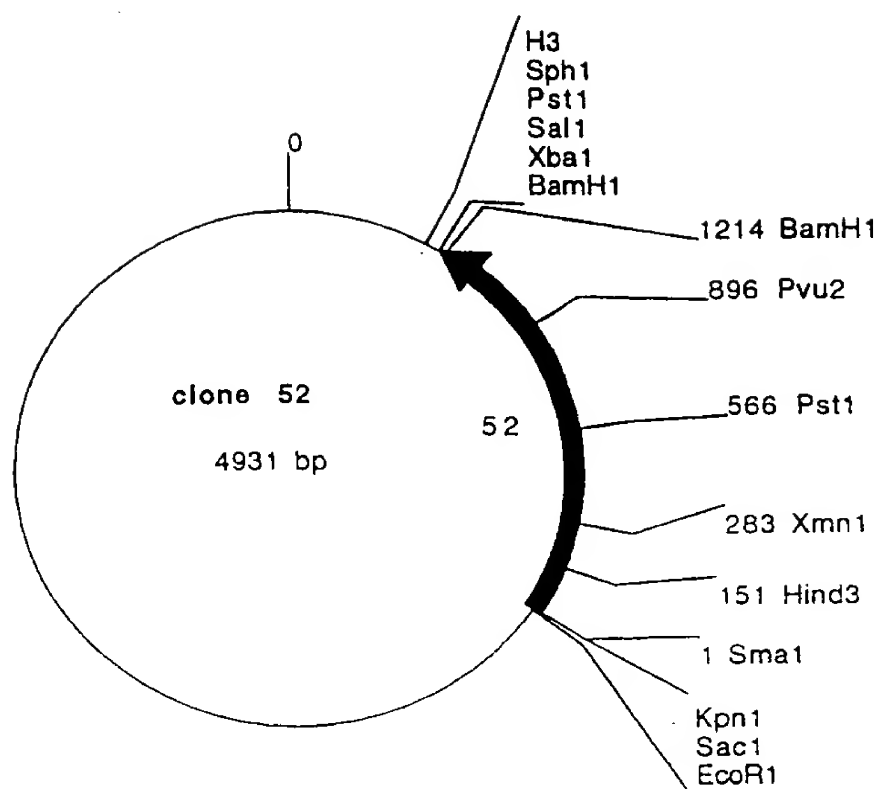


Figure 2

Comments/References: 52= 3' side of S5 (AIMSH3) 1244bp in pUC18/Sma1

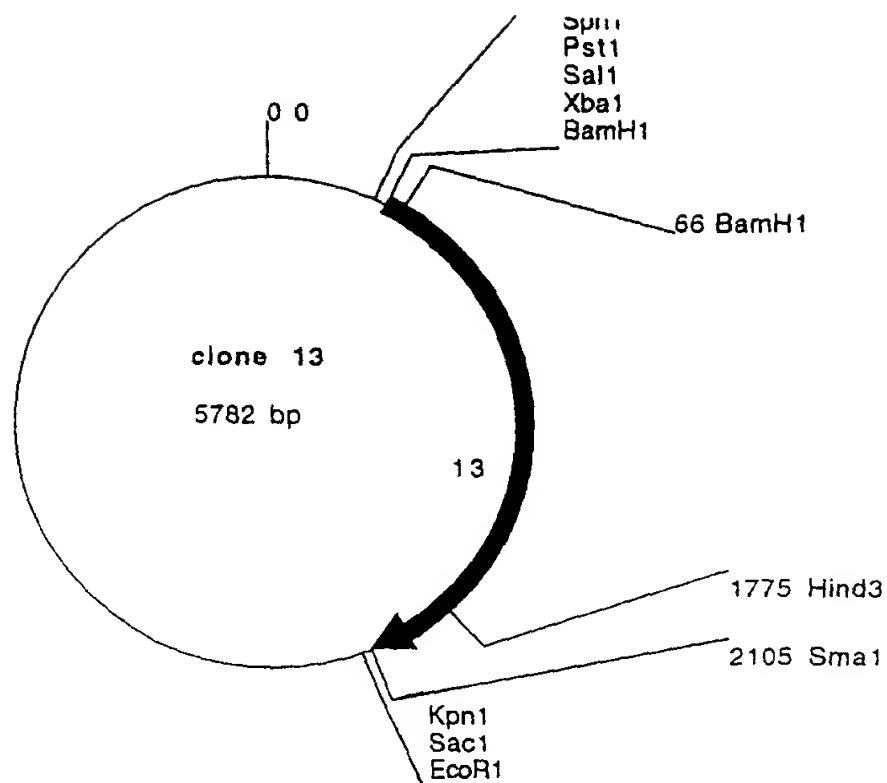


Figure 3

Comments/References: 13 = 3' side of S5 (AtMSH3) 2104bp in pUC18/SmaI

SEQUENCE

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81	gattacgaataaagcaatt atg ggc aag caa aag cag cag acg att tct cgt ttc ttc gct ccc	144
1	m g k q k q q t i s r f a p	15
145	aaa ccc aaa tcc ccc act cac gaa ccc aat ccc gta gcc gaa tca tca aca ccc cca ccc	204
16	k p k s p t h e p n p v a e s s t p p p	35
205	aag ata tcc gcc act gta tcc ttc tct cct tcc aag cgt aag ctt ctc tcc gac cac ctc	264
36	k i s a t v s f s p s k r k l l s d h l	55
265	gcc gcc gcc tca ccc aaa aag cct aaa ctt tct cct cac act caa aac cca gta ccc gat	324
56	a a a s p k k p k l s p h t q n p v p d	75
325	ccc aat tta cac caa aga ttt ctc cag aga ttt ctg gaa ccc tcg ccc gag gaa tat gtt	384
76	p n l h q r f l q r f l e p s p e e y v	95
385	ccc gaa acg tca tca tcc agg aaa tac aca cca ttg gaa cag caa gtg gtg gag cta aag	444
96	p e t s s s r k y t p l e q v v e l k	115
445	agc aag tac cca gat gtg gtt ttg atg gtg gaa gtt ggt tac agg tac aga ttc ttc gga	504
116	s k y p d v v l m v e v g y r y r f f g	135
505	gaa gac gcc gag atc gca gcc gtg ttg ggt att tac gct cat atg gat cac aat ttc	564
136	e d a e i a a r v l g i y a h m d h n f	155
565	atg acg gcc agt gtg cca aca ttt cga ttg aat ttc cat gtg aga aga ctg gtg aat gca	624
156	m t a s v p t f r l n f h v r l v n a	175
625	gga tac aag att ggt gta gtg aag cag act gaa act gca gcc att aag tcc cat ggt gca	684
176	g y k i g v v k q t e t a a i k s h g a	195
665	aac cgg acc gcc cct ttt ttc cgg gga ctg tcc gcc ttg tat acc aaa gcc acg ctt gaa	744
196	n r t g p f f r g l s a l y t k a t l e	215
745	gcc gct gag gat ata agt ggt ggt ggt gaa gaa ggt ttt ggt tca cag agt aat	804
216	a a e d i s g g c g e e g f g s q s n	235
805	ttc ttg gtt tgt gtt gat gag aga gtt aag tcc gag aca tta gcc tgt ggt att gaa	864
236	f l v c v v d e r v k s e t l g c g i e	255
865	atg agt ttt gat gtt aga gtc ggt gtt ggc gtt gaa att tcc aca ggt gaa gtt gtt	924
256	m s f d v r v g v v g v e i s t g e v v	275

Figure 4

Q4207 SE2656D

925	TAT	GAA	GAG	TTC	AAT	GAT	AAT	TTC	ATG	AGA	AGT	GGA	TTA	GAG	GCT	GTG	ATT	TTG	AGC	TTG	984
276	Y	E	E	F	N	D	N	F	M	R	S	G	L	E	A	V	I	L	S	L	295
985	TCA	CCA	GCT	GAG	CTG	TTG	CTT	GGC	CAG	CCT	CTT	TCA	CAA	CA	ACT	GAG	AAG	TTT	TTG	GTG	1044
296	S	P	A	E	L	L	L	G	Q	P	L	S	Q	Q	T	E	K	F	L	V	315
1045	GCA	CAT	GCT	GGA	CCT	ACC	TCA	AAC	GTT	CGA	GTG	GAA	CGT	GCC	TCA	CTG	GAT	TGT	TTT	AGC	1104
316	A	M	A	G	P	T	S	N	V	R	V	E	R	A	S	L	D	C	F	S	335
1105	AAT	GGT	AAT	GCA	GTA	GAT	GAG	GTT	ATT	TCA	TTA	TGT	GAA	AAA	ATC	AGC	GCA	GGT	AAC	TTA	1164
336	N	G	N	A	V	D	E	V	I	S	L	C	E	K	I	S	A	G	N	L	355
1165	GAA	GAT	GAT	AAA	GAA	ATG	AAG	CTG	GAG	GCT	GCT	GAA	AAA	GGA	ATG	TCT	TGC	TTG	ACA	GTT	1224
356	E	D	D	K	E	M	K	L	E	A	A	E	K	G	M	S	C	L	T	V	375
1225	CAT	ACA	ATT	ATG	AAC	ATG	CCA	CAT	CTG	ACT	GTT	CAA	GCC	CTC	GCC	CTA	ACG	TTT	TGC	CAT	1284
376	H	T	I	M	N	M	P	H	L	T	V	Q	A	L	A	L	T	F	C	H	395
1285	CTC	AAA	CAG	TTT	GGA	TTT	GAA	AGG	ATC	CTT	TAC	CAA	GGG	GCC	TCA	TTT	CGC	TCT	TTG	TCA	1344
396	L	K	Q	F	G	F	E	R	I	L	Y	Q	G	A	S	F	R	S	L	S	415
1345	AGT	AAC	ACA	GAG	ATG	ACT	CTC	TCA	GCC	AAT	ACT	CTG	CAA	CAG	TTG	GAG	GTT	GTG	AAA	AAT	1404
416	S	N	T	E	M	T	L	S	A	N	T	L	Q	Q	L	E	V	V	K	N	435
1405	AAT	TCA	GAT	GGA	TCG	GAA	TCT	GGC	TCC	TTA	TTC	CAT	AAT	ATG	AAT	CAC	ACA	CTT	ACA	GTA	1464
436	N	S	D	G	S	E	S	G	S	L	F	H	N	M	N	H	T	L	T	V	455
1465	TAT	GCT	TCC	AGG	CTT	CTT	AGA	CAC	TGG	GTG	ACT	CAT	CCT	CTA	TGC	GAT	AGA	AAT	TTG	ATA	1524
456	Y	G	S	R	L	L	R	H	W	V	T	H	P	L	C	D	R	N	L	I	475
1525	TCT	GCT	CGG	CTT	GAT	GCT	GTT	TCT	GAG	ATT	TCT	GCT	TGC	ATG	GGA	TCT	CAT	AGT	TCT	TCC	1584
476	S	A	R	L	D	A	V	S	E	I	S	A	C	M	G	S	H	S	S	S	495
1585	CAG	CTC	AGC	AGT	GAG	TTG	GTT	GAA	GAA	GGT	TCT	GAG	AGA	GCA	ATT	GTA	TCA	CCT	GAG	TTT	1644
496	Q	L	S	S	E	L	V	E	E	G	S	E	R	A	I	V	S	P	E	F	515
1645	TAT	CTC	GTG	CTC	TCC	TCA	GTC	TTG	ACA	GCT	ATG	TCT	AGA	TCA	TCT	GAT	ATT	CAA	CGT	GGA	1704
516	Y	L	V	L	S	S	V	L	T	A	M	S	R	S	S	D	I	Q	R	G	535
1705	ATA	ACA	AGA	ATC	TTT	CAT	CGG	ACT	GCT	AAA	GCC	ACA	GAG	TTC	ATT	GCA	GTT	ATG	GAA	GCT	1764
536	I	T	R	I	F	H	R	T	A	K	A	T	E	F	I	A	V	M	E	A	555
1765	ATT	TTA	CTT	GGG	GGG	AAG	CAA	ATT	CAG	CGG	CTT	GGC	ATA	AAG	CAA	GAC	TCT	GAA	ATG	AGG	1824
556	I	L	L	A	G	K	Q	I	Q	R	L	G	I	K	Q	D	S	E	M	R	575

Figure 4 (Continued)

DQ420T" 6E262560

1825	AGT	ATG	CAA	TCT	GCA	ACT	GTG	CGA	TCT	ACT	CTT	TTG	AGA	AAA	TTG	ATT	TCT	GTT	ATT	TCA	1884	
576	S	M	Q	S	A	T	V	R	S	T	L	L	R	K	L	I	S	V	I	S	595	
1885	TCC	CCT	GTT	GTG	GTT	GAC	AAT	GCC	GGA	AAA	CTT	CTC	TCT	GCC	CTA	AAT	AAG	GAA	GCG	GCT	1944	
596	S	P	V	V	V	D	N	A	G	K	L	L	S	A	L	N	K	E	A	A	615	
1945	GTT	CGA	GGT	GAC	TTG	CTC	GAC	ATA	CTA	ATC	ACT	TCC	AGC	GAC	CAA	TTT	CCT	GAG	CTT	GCT	2004	
616	V	R	G	D	L	L	D	I	L	I	T	S	S	D	Q	F	P	E	L	A	635	
2005	GAA	GCT	CGC	CAA	GCA	GTT	TTA	GTC	ATC	AGG	GAA	AAG	CTG	GAT	TCC	TCG	ATA	GCT	TCA	TTT	2064	
636	E	A	R	Q	A	V	L	V	I	R	E	K	L	D	S	S	I	A	S	F	655	
2065	CGC	AAG	AAG	CTC	GCT	ATT	CGA	AAT	TTG	GAA	TTT	CTT	CAA	GTG	TCG	GGG	ATC	ACA	CAT	TTG	2124	
656	R	K	K	L	A	I	R	N	L	E	F	L	Q	V	S	G	I	T	H	L	675	
2125	ATA	GAG	CTG	CCC	GTT	GAT	TCC	AAG	GTC	CCT	ATG	AAT	TGG	GTG	AAA	GTA	AAT	AGC	ACC	AAG	2184	
676	I	E	L	P	V	D	S	K	V	P	H	N	W	V	K	V	N	S	T	K	695	
2185	AAG	ACT	ATT	CGA	TAT	CAT	CCC	CCA	GAA	ATA	GTA	GCT	GGC	TTG	GAT	GAG	CTA	GCT	CTA	GCA	2244	
696	K	T	I	R	Y	H	P	P	E	I	V	A	G	L	D	E	L	A	L	A	715	
2245	ACT	GAA	CAT	CTT	GCC	ATT	GTG	AAC	CGA	GCT	TCG	TGG	GAT	AGT	TTC	CTC	AAG	AGT	TTC	AGT	2304	
716	T	E	H	L	A	I	V	N	R	A	S	W	D	S	F	L	K	S	F	S	735	
2305	AGA	TAC	TAC	ACA	GAT	TTT	AAG	GCT	GCC	GTT	CAA	GCT	CTT	GCT	GCA	CTG	GAC	TGT	TTG	CAC	2364	
736	R	Y	Y	T	D	F	K	A	A	V	Q	A	L	A	A	L	D	C	L	H	755	
2365	TCC	CTT	TCA	ACT	CTA	TCT	AGA	AAC	AAG	AAC	TAT	GTC	CGT	CCC	GAG	TTT	GTG	GAT	GAC	TGT	2424	
756	S	L	S	T	L	S	R	N	K	N	Y	V	R	P	E	F	V	D	D	C	775	
2425	GAA	CCA	GTT	GAG	ATA	AAC	ATA	CAG	ACA	ATT	GGT	CGT	CAT	CCT	GTA	CTG	GAG	ACT	ATA	TTA	CAA	2484
776	E	P	V	E	I	N	I	Q	T	I	S	G	R	H	P	V	L	E	T	I	L	795
2485	GAT	AAC	TTT	GTC	CCA	AAT	GAC	ACA	ATT	TTG	CAT	GCA	GAA	GGG	GAA	TAT	TGC	CAA	ATT	ATC	2544	
796	D	N	F	V	P	N	D	T	I	L	H	A	E	G	E	Y	C	Q	I	I	815	
2545	ACC	GGA	CCT	AAC	ATG	GGA	GGA	AAG	AGC	TGC	TAT	ATC	CGT	CAA	GTT	GCT	TTA	ATT	TCC	ATA	2604	
816	T	G	P	N	M	G	G	K	S	C	Y	I	R	Q	V	A	L	I	S	I	835	
2605	ATG	GCT	CAG	GTT	GGT	TCC	TTT	GTA	CCA	GCG	TCA	TTC	GCC	AAG	CTG	CAC	GTG	CTT	GAT	GGT	2664	
836	M	A	Q	V	G	S	F	V	P	A	S	F	A	K	L	H	V	L	D	G	855	
2665	GTT	TTC	ACT	CGG	ATG	GGT	GCT	TCA	GAC	AGT	ATC	CAG	CAT	GGC	AGA	AGT	ACC	TTT	CTA	GAA	2724	
856	V	F	T	R	M	G	A	S	D	S	I	Q	H	G	R	S	T	F	L	E	875	

Figure 4 (Continued)

004201" 66262550

2725	GAA	TTA	AGT	GAA	GGG	TCA	CAC	ATA	ATC	AGA	ACC	TGT	TCT	TCT	CGT	TCG	CTT	GTT	ATA	TTA	2784
876	E	L	S	E	A	S	H	I	I	R	T	C	S	S	R	S	L	V	I	L	895
2785	GAT	GAG	CTT	GGA	AGA	GGC	ACT	AGC	ACA	CAC	GAC	GGT	GTA	GCC	ATT	GCC	TAT	GCA	ACA	TTA	2844
896	D	E	L	G	R	G	T	S	T	H	D	G	V	A	I	A	Y	A	T	L	915
2845	CAG	CAT	CTC	CTA	GCA	GAA	AAG	AGA	TGT	TTG	CTT	CTT	TTT	GTC	ACG	CAT	TAC	CCT	GAA	ATA	2904
916	Q	H	L	L	A	E	K	R	C	L	V	L	F	V	T	H	Y	P	E	I	935
2905	GCT	GAG	ATC	AGT	AAC	GGA	TTC	CCA	GGT	TCT	GTT	GGG	ACA	TAC	CAT	GTC	TCG	TAT	CTG	ACA	2964
936	A	E	I	S	N	G	F	P	G	S	V	G	T	Y	H	V	S	Y	L	T	955
2965	TTG	CAG	AAG	GAT	AAA	GGC	AGT	TAT	GAT	CAT	GAT	GAT	GTG	ACC	TAC	CTA	TAT	AAG	CTT	GTG	3024
956	L	Q	K	D	K	G	S	Y	D	H	D	D	V	T	Y	L	Y	K	L	V	975
3025	CGT	GGT	CTT	TGC	AGC	AGG	AGC	TTT	GGT	TTT	AAG	GTT	GCT	CAG	CTT	GCC	CAG	ATA	CCT	CCA	3084
976	R	G	L	C	S	R	S	F	G	F	K	V	A	Q	L	A	Q	I	P	P	995
3085	TCA	TGT	ATA	CGT	CGA	GCC	ATT	TCA	ATG	GCT	GCA	AAA	TTG	GAA	GCT	GAG	GTA	CGT	GCA	AGA	3144
996	S	C	I	R	A	I	S	M	A	A	K	L	E	A	E	V	R	A	R		1015
3145	GAG	AGA	AAT	ACA	CGC	ATG	GGA	GAA	CCA	GAA	GGA	CAT	GAA	CCG	AGA	CCG	GCA	GAA	GAA	GAA	3204
1016	E	R	N	T	R	M	G	E	P	E	G	H	E	E	P	R	G	A	E	E	1035
3205	TCT	ATT	TCG	GCT	CTA	GGT	GAC	TTG	TTT	GCA	GAC	CTG	AAA	TTT	GCT	CTC	TCT	GAA	GAG	GAC	3264
1036	S	I	S	A	L	G	D	L	F	A	D	L	K	F	A	L	S	E	E	D	1055
3265	CCT	TGG	AAA	GCA	TTC	GAG	TTT	TTA	AAG	CAT	GCT	TGG	AAG	ATT	GCT	GGC	AAA	ATC	AGA	CTA	3324
1056	P	W	K	A	F	E	F	L	K	H	A	W	K	I	A	G	K	I	R	L	1075
3325	AAA	CCA	ACT	TGT	TCA	TTT	TGA	TTTAATCTTAACATTATAGCAACTGCAAGGCTTGTGATCATCTGTTAGTTGCG													3397
1076	K	P	T	C	S	F	*														1082
3398	TACTAACTT	ATG	TGT	ATT	AGT	ATA	ACA	AGA	AAA	GAG	AAT	TAG	AGAG	ATG	GAT	TCT	AAT	CCG			3458
1																				5	
3459	GTG	TTG	CAG	TAC	ATC	TTT	TCT	CCA	CCC	GCA	TAA	AAAAAAAAAAAAAAAAAAAAAAAAAAAA									3522
6	V	L	Q	Y	I	F	S	P	P	A	*										16

Figure 4 (Continued)

004201" 6E262560

Figure 5

```

MSH3_AL 1 --MSKQK-----QOTISREFAPKSP-TH--PMFVASSSTPPK-----ISAVSPSPSKMALL
MSH3_SC 1 MVIENEPKLVLLRAKSSANKRPILLNLTIMAGQPTISRPKKA[K]SELTHKQEQVAVGMGAGSEKICLDTUEKDNLSVASPTVIMUSPTLKS

MSH3_AL 52 SDHLAAASPKKPKL8PHQ[P]VPDPNINQRPLQVLEP-----SPEYVVPETSS--SRKYTPLEQVAVKSKSPDVPVVEVGY[P]V
MSH3_SC 96 VSYKNSKNSKSTSGTST[P]PDIYAKKLURIMKMSDENVEADEDEE[GE]DFVKKKAKKSP[TA]RLTPLDKQVADK[NA]HARDKPLVIMVGY[P]V

MSH3_AL 134 [P]SDAEIAARVCGIYAH-----MQRN-----PTASVPTPLNPHVRLVMAOYKIQVYK[P]TEVAKNSG--GAMNTGPP[P]GLSALY[P]KA
MSH3_SC 191 PAEDAVTVSRILH[K]KLVPGKLTIDESNPQUUNHKQPAYCSPPOVRLNVHLERLVHNLKVAVK[SA]ETSAYKKHDPGASESSVPFRKISMV[P]KA

MSH3_AL 213 [L]EAASDISGCGGEGEP[Q]SQSNPLVCVVDKRVKSET[P]UCGIENSFUVKVGVO[P]EISTEVAVK[P]EPND-PPMRSG[SA]VLLS9PA[EL]LG-Q[P]
MSH3_SC 286 [P]QVNSTPVLN-----GKR-----ILGDTNSIWA[CS]RDVHQGVAKYSLISUNLNMGEVAVDEFE[P]BLADEK[SO]IA[K]Y[P]EVEVNTLU

MSH3_AL 306 [G]BQQTER[P]LVAAHQ[P]TSNVVRVERASLDCFSNGNAVDV[P]V[CS]CKISAGNLEDKMKLBAEKGNKCLTVMTIMNMPHLTVOALALT[P]CBLKOPQ
MSH3_SC 368 [P]LVAAKE[P]KDISC[P]LHKQYDLEEDUVQAIKVMNEK[P]Q[CS]P[L]-----IRLVSKLYS[P]V[VE]YN,

MSH3_AL 401 [P]ERILYOGASPKSLSSMTET[P]GSA[P]T[P]Q[P]EVVKNNSDGSES[GS]LFNNMNH[TL]VIGSR[P]L[P]R[NA]VT[P]L[C]CKML[IS]ARLDVASE[IS]ACMUSHSS
MSH3_SC 428 [N]EQVMLIPSIYSPPAKINHL[P]DP[NS]Q[CS]DIPTHD--GK-GS[P]MLLDH[NA]ST[P]GL[EM]AR[P]L[P]VDPVHQ[RE]LEDAIEC[P]TSEINNS--

MSH3_AL 496 [L]SSELVEEGSRRAIVSPHYLVLSVLTAMSNSSDIQGITRIPRR[CA]KATEPIAVMEAL[L]LAKQIQRLGKQDSMM[SS]Q[OS]-ATVNST[P]L[P]K
MSH3_SC 517 -----IPPE[SL]NQMLNHT[P]DL[ST]LNRIMYQ[CS]TSKKEVYVYLKQ[IT]SPVDNYKMBQSYLSEHP[SS]DORIUQ[OS]P[P]L[P]M

MSH3_AL 590 [P]ISV[IS]SPVVVOMAOKL[P]GAL[K]K[NA]VRG-----DLLDYLITS-SQPPPLAEARQAVLVIREK[P]DSSIAS[P]R[K]CAI[RM]P[P]ELQVSGITLIELP
MSH3_SC 591 [P]FSELNELSTTQLP[P]P[P]TMINRVSIVMEKNSOKQVMD[P]FNLNND[CS]EGIIKIQRESSESV[Q]CKEELAEIRKY[P]KRPYENENDEVDYLIEVKN[NS]

MSH3_AL 680 VDSKVP[MM]NVK[VS]CKKTIRY[P]PPEI[VA]GLDE[P]ALATE[P]HAIVNKASWDS[P]CK[P]9[P]RY[P]CP[K]AAVQA[CA]L[OC]LH[SS]STLS[P]MRYVRP[P]VQDU
MSH3_SC 686 QIKDLP[DD]IKVNN[P]KMAVSRVTPPTPTQXLTQKDEYYKDL[LI]NESELQYK[P]ELNKITAEY[TE]LEK[IT]LM[CA]QYDCILSLAATSCNNVAVRP[P]VQDU

MSH3_AL 775 CEPVEINIQSORHPVLE[P]TIGQDNFVPHDTILHAPQY[C]QITGP[PH]GCKS-VIROVAL[P]I[HA]QV[GS]PVP[P]9[P]PAL[EN]VLDOV[P]P[RM]CA[SS]S[P]Q[MS]
MSH3_SC 783 QO--AHIAKNARNP[IES]-DOVHYVNDIMNS[P]ENGKINILITGP[PH]GCKS-VIROVAL[P]I[HA]QV[GS]PVP[P]E[IR]E[SI]YENL[TR]IGAB[P]D[P]I[NS]

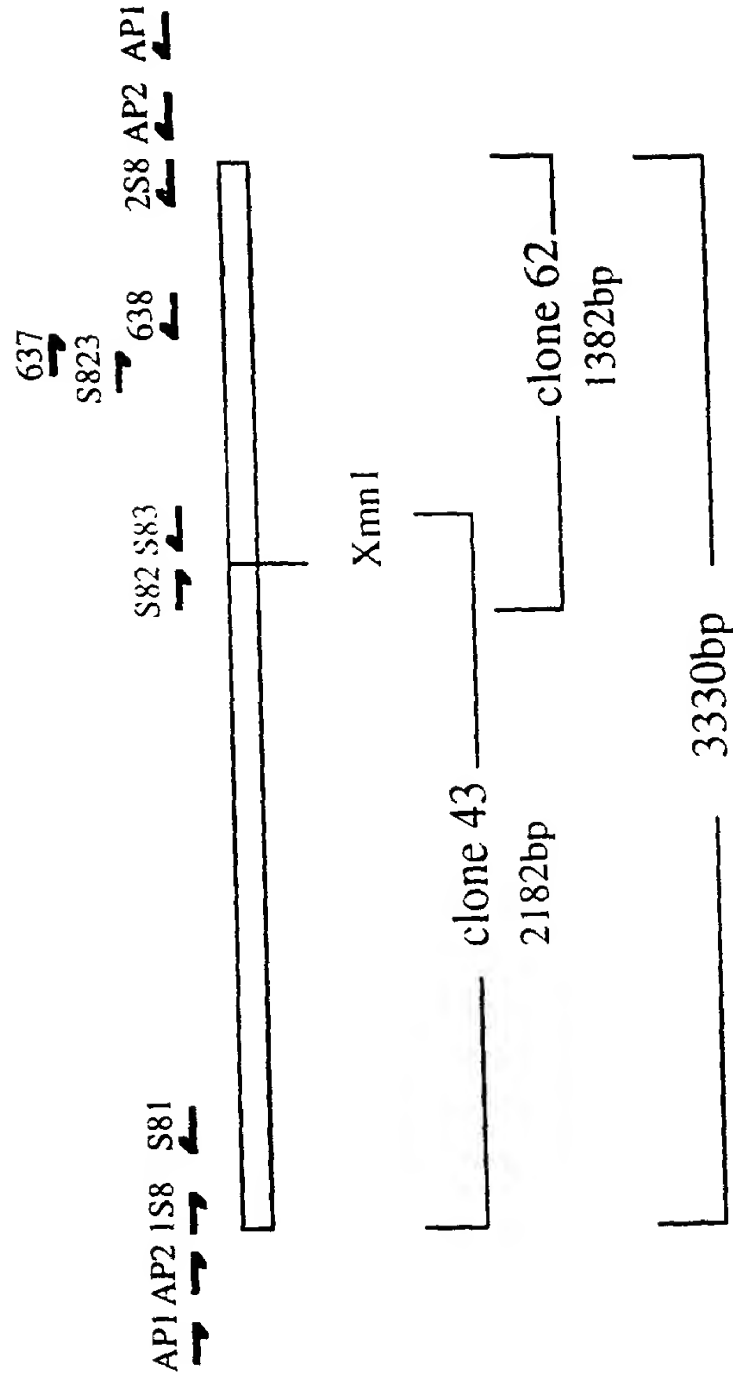
MSH3_AL 870 RSTPLRELKSKASHIR[TC]SSRS[V]I[DE]LGRGTS[TH]DGV[IA]YATLQHLIAEKRC-[V]P[P]V[P]HYPIA[BI]SNGP[GS]VQTVHVS[TL]LQKDKQSY
MSH3_SC 873 DSTPKVEMLDILHILKNCNARSELLEDEVGRTJPHDGINISVILIKYFSELSDC[P]P[AI]G[P]TH[P]P[L]QLEK[SS]--PLIRNM[P]MDIVERO[Q]--TQK

MSH3_AL 964 QMDDUTIYKGV[SG]TC[SR]SPGPKVQAQI[PP]SC[P]HRAISMAAK[P]KAEVMARENHTKMQEP[EO]HE[P]ROA[ES]ISAL[P]DLPAD[P]K[P]A[P]J[P]E[P]M[P]K
MSH3_SC 963 QMNSI[P]P[SY]K[K]K[GL]TYN[ST]GMN[VA]KCARLDKDIINRAP[SI]SE[P]R[K]ESIN-----EDALK[Q]--ES[SA]KAI[CS]SDM---

MSH3_AL 1059 APEPLAHAWK[P]AOKIN[P]KPTC[P]P---
MSH3_SC 1032 -----P[AT]D[P]KAKL[SL]D[IN]

```


Figure 6



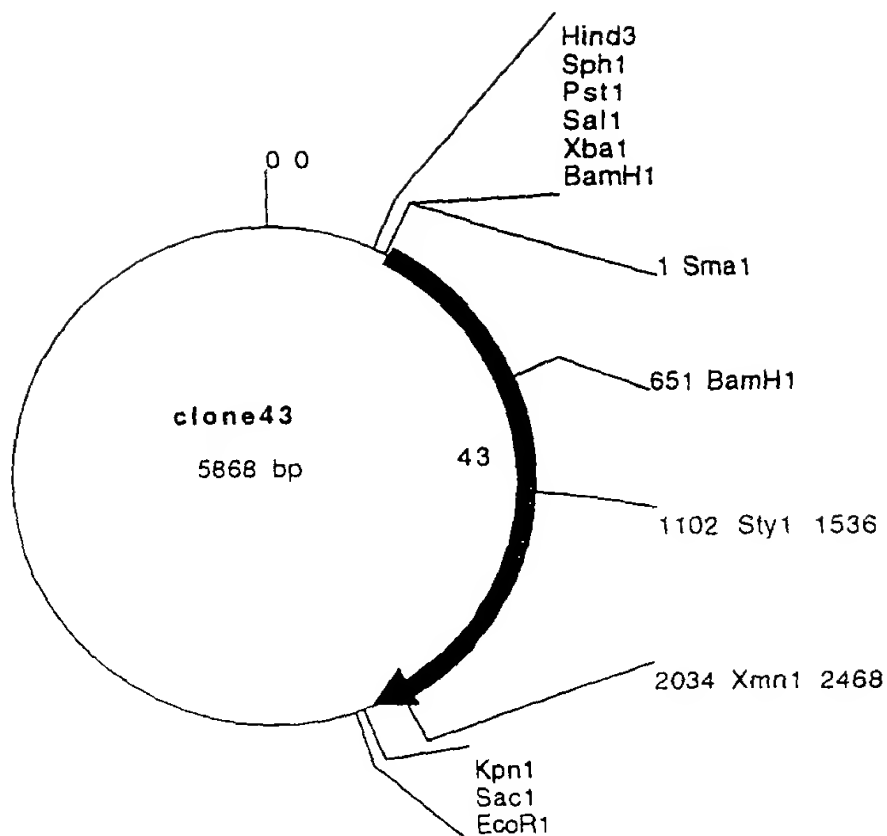


Figure 7

Comments/References: 43= 5' side of S8 (AtMSH6) 2182 bp in pUC18/Sma1

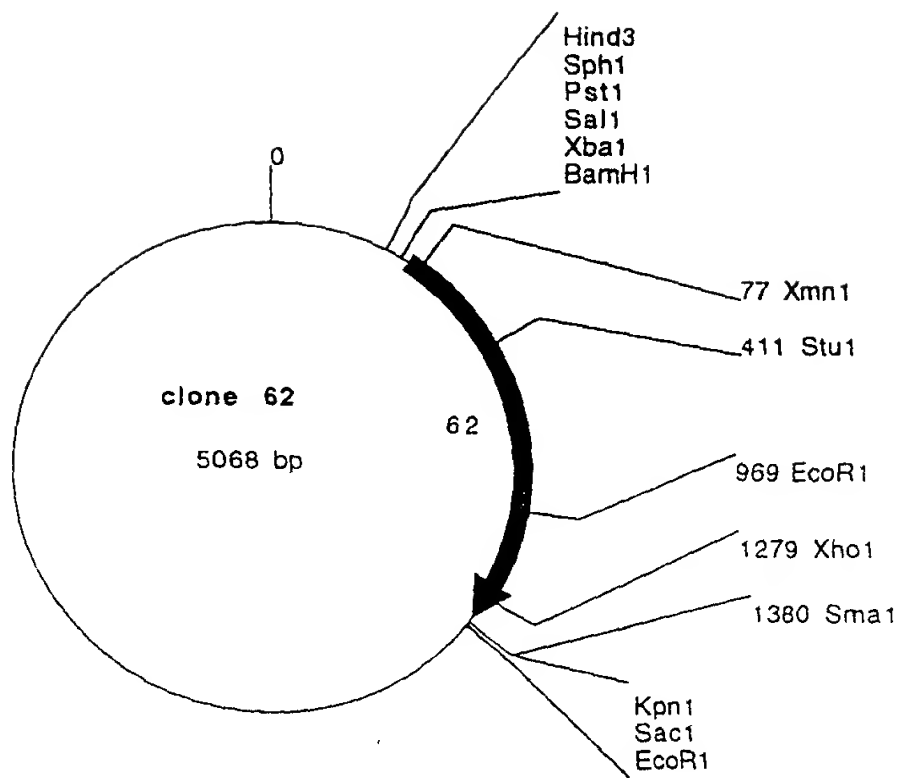


Figure 8

Comments/References: 62= 3' side of S8 (AtMSH6) 1379bp in pUC18/Sma1

Sequence

1	AAAAGTTGAGCCCTGAGGAGTATCGTTTCGCCCATTTCTACGACGCAAGCGAAATTTTGGCGCCAATCTTTCCCCCC	80
81	TTTCGAATTCTCTCAGCTCRAAAACATCGTTTCTCTCTCACTCTCTCTCACAATTCACAAAAA	153
1		4
154	AGA TCG ATT TTG TCT TTC CAA AAA CCC ACC GCG GCG ACT ACG AAG GGT TTG GTT TCC	213
5	R S I L S F F Q K P T A A T T K G L V S	24
214	GGC GAT GCT GCT AGC GGC GGC GGC AGC GGA CCA CGA TTT AAT GTG AAG GAA GGG	273
25	G D A A S G G G G S G G P R F N V R E G	44
274	GAT GCT AAA GGC GAC GCT TCT GTA CGT TTT GCT GTT TCG AAA TCT GTC GAT GAG GTT AGA	333
45	D A K G D A S V R F A V S K S V D E V R	64
334	GGA ACG GAT ACT CCA CCG GAG AAG GTT CCG CGT GTC CTG CCG TCT GGA TTT AAG CCG	393
65	G T D T P P E K V P P R R V L P S G F K P	84
394	GCT GAA TCC GCC GST GAT GCT TCG TCC CTG TCC AAT ATT ATG CAT AAG TTT GTA AAA	453
85	A E S A G D A S S L F S N I M H K F V K	104
454	GTC GAT GAT CGA GAT TGT TCT GGA GAG AGG AGC CGA GAA GAT GTT CCG CTG AAT GAT	513
105	V D D R D C S G E R S R E D V V P L N D	124
514	TCA TCT CTA TGT ATG AAG GCT AAT GAT GTT ATT CCT CAA TTT CGT TCC AAT AAT GGT AAA	573
125	S S L C M K A N D V I P Q F R S N N G K	144
574	ACT CAA GAA AGA AAC CAT GCT TTT AGT TTC AGT GGG AGA GCT GAA CTT AGA TCA GTA GAA	633
145	T Q E R N H A F S F S G R A E L R S V E	164
634	GAT ATA GGA GTA GAT GGC GAT GTT CCT GGT CCA GAA ACA CCA GGG ATG CGT CCA CGT GCT	693
165	D I G V D G D V P G P E T P G M R P R A	184
694	TCT CGC TTG AAG CGA GTT CTG GAG GAT GAA ATG ACT TTT AAG GAG GAT AAG GTT CCT GTA	753
185	S R L K R V L E D E M T F K E D K V P V	204
754	TTG GAC TCT AAC AAA AGG CTG AAA ATG CTC CAG GAT CCG GTT TGT GGA GAG AAG AAA GAA	813
205	L D S N K R L L K M L Q D P V C G E K K E	224
814	GTA AAC GAA GGA ACC AAA TTT GRA TGG CTT GAG TCT TCT CGA ATC AGG GAT GCC AAT AGA	873
225	V N E G T K F E W L E S S R I R D A N R	244
874	AGA CGT CCT GAT GAT CCC CTT TAC GAT AGA AAG ACC TTA CAC ATA CCA CCT GAT GTT TTC	933
245	R R P D D P L Y D R K T L H I P P D V F	264

Figure 9

DECT "SEES60"

934	ARG AAA ATG TCT GCA TCA CAA AAG CAA TAT TGG AGT GTT AAG AGT GAA TAT ATG GAC ATT	993
265	K K M S A S Q K Q Y W S V K S E Y M D I	284
996	GTG CTT TTC TTT AAA GTG GGG AAA TTT TAT GAG CTG TAT GAG CTA GAT GCG GAA TTA GGT	1053
285	V L F F K V G K K F Y E L Y E L D A E L G	304
1054	CAC AAG GAG CTT GAC TGG AAG ATG ACC ATG AGT GGT GTG GGA AAA TGC AGA CAG GTT GGT	1113
305	H K E L D W K M T M S G V G K C R Q V G	324
1114	ATC TCT GAA AGT GGG ATA GAT GAG GCA GTG CAA AAG CTA TTA GCT CGT GGA TAT AAA GTT	1173
325	I S E S G I D E A V Q K L L A R G Y K V	344
1174	GGA CGA ATC GAG CAG CTA GAA ACA TCT GAC CAA GCA AAA GCC AGA GGT GCT AAT ACT ATA	1233
345	G R I E Q L E T S D Q A K A R G A N T I	364
1234	ATT CCA AGG AAG CTA GTT CAG GTA TTA ACT CCA TCA ACA GCA AGC GAG GGA AAC ATC GGG	1293
365	I P R K L V Q V L T P S T A S E G N I G	384
1294	CCT GAT GCC GTC CAT CTT CTT GCT ATA AAA GAG ATC AAA ATG GAG CTA CAA AAG TGT TCA	1353
385	P D A V H L A I K E I K M E L Q K C S	404
1354	ACT GTG TAT GGA TTT GCT TTT GCT TTT GCT GCT TTT GCT TTT TGG GTT GGG TCC ATC	1413
405	T V Y G F A F V D C A A L R F V G S I	424
1414	AGC GAT GAT GCA TCA TGT GCT CTT GGA GCG TTA TTG ATG CAG GTT TCT CCA AAG GAA	1473
425	S D D A S C A A L G A L L M Q V S P K E	444
1474	GTG TTA TAT GAC AGT AAA GGG CTA TCA AGA GAA GCA CAA AAG GCT CTA AGG AAA TAT ACG	1533
445	V L Y D S K G L S R E A Q K A L R K Y T	464
1534	TTG ACA GGG TCT ACG GCG GTA CAG TTG GCT CCA GTA CCA CAA GTA ATG GGG GAT ACA GAT	1593
465	L T G S T A V Q L A P V P Q V M G D T D	484
1594	GCT GCT GGA GTT AGA AAT ATA ATA GAA TCT AAC GGA TAC TTT ANA GGT TCT TCT GAA TCA	1653
485	A G V R N I I E S N G Y F K G S S E S	504
1654	TGG AAC TGT GCT GTT GAT GGT CTA AAT GAA TGT GAT GTT GCC CTT AGT GCT CTT GGA GAG	1713
505	W N C A V D G L N E C D V A L S A L G E	524
1714	CTA ATT AAT CAT CTG TCT AGG CTA AAG CTA GAT GTA CTT AAG CAT GGG GAT ATT TTT	1773
525	L I N H L S R L K L E D V L K H G D I F	544
1774	CCA TAC CAA GTT TAC AGG GGT TGT CTC AGA ATT GAT GGC CAG ACG ATG GTA AAT CTT GAG	1833
545	P Y Q V Y R G C L R I D G Q T M V N L E	564

Figure 9 (Continued)

SEQUENCE

1834	ATA	TTT	AAC	AAT	AGC	TGT	GAT	GGT	GAT	GGT	CCT	TCA	GGG	ACC	TTG	TAC	AAA	TAT	CTT	GAT	AAC	1893
565	I	F	N	N	S	C	D	G	G	G	P	S	G	T	L	Y	K	Y	L	D	N	584
1894	TGT	GTT	AGT	CCA	ACT	GGT	AAG	CGA	CTC	TTA	AGG	AAT	TGG	ATC	TGC	CAT	CCA	CTC	AAA	GAT	1953	
585	C	V	S	P	T	G	K	R	L	L	R	N	W	I	C	H	P	L	K	D	604	
1954	GTA	GAA	AGC	ATC	AAT	AAA	CGG	CTT	GAT	GTA	GTT	GAA	GAA	TTC	ACG	GCA	AAC	TCA	GAA	AGT	2013	
605	V	E	S	I	N	K	R	L	D	V	V	E	E	F	T	A	N	S	E	S	624	
2014	ATG	CAA	ATC	ACT	GGC	CAG	TAT	CTC	CAC	AAA	CTT	CCA	GAC	TTA	GAA	AGA	CTG	CTC	GGA	CGC	2073	
625	M	Q	I	T	G	Q	Y	L	H	K	L	P	D	L	E	R	L	L	G	R	644	
2074	ATC	AAG	TCT	AGC	GTT	CGA	TCA	TCA	GCC	TCT	TGT	TTG	CCT	GCT	CTT	CTG	GGG	AAA	AAA	GTG	2133	
645	I	K	S	S	V	R	S	S	A	S	V	L	P	A	L	L	G	K	K	V	664	
2134	CTG	AAA	CAA	CGA	GTT	AAA	GCA	TTT	GGG	CAA	ATT	CTG	AAA	GGG	TTC	AGA	AGT	GGA	ATT	GAT	2193	
665	L	K	Q	R	V	K	A	F	G	Q	I	V	K	G	F	R	S	G	I	D	684	
2194	CTG	TTG	TTG	GCT	CTA	CAG	AAG	GAA	TCA	AAT	ATG	ATG	AGT	TTG	CTT	TAT	AAA	CTC	TGT	AAA	2253	
685	L	L	A	L	Q	K	E	S	N	M	S	L	L	L	Y	K	L	C	K		704	
2254	CTT	CCT	ATA	TTA	GTA	GGA	AAA	AGC	GGG	CTA	GAG	TTA	TTT	CTT	TCT	CAA	TTC	GAA	GCA	GCC	2313	
705	L	P	I	L	V	G	K	S	G	L	E	L	F	L	S	Q	F	E	A	A	724	
2314	ATA	GAT	AGC	GAC	TTT	CCA	AAT	TAT	CAG	AAC	CAA	GAT	GTG	ACA	GAT	GAA	AAC	GCT	GAA	ACT	2373	
725	I	D	S	D	F	P	N	Y	Q	N	Q	D	V	T	D	E	N	A	E	T	744	
2374	CTC	ACA	ATA	CTT	ATC	GAA	CTT	TTT	ATC	GAA	AGA	GCA	ACT	CAA	TGG	TCT	GAG	GTC	ATT	CAC	2433	
745	L	T	I	L	I	E	L	F	I	E	R	A	T	Q	W	S	E	V	I	H	764	
2434	ACC	ATA	AGC	TGC	CTA	GAT	GTC	CTG	AGA	TCT	TTT	GCA	ATC	GCA	GCA	AGT	CTC	TCT	GCT	GGA	2493	
765	T	I	S	C	L	D	V	L	R	S	F	A	I	A	A	S	L	S	A	G	784	
2494	AGC	ATG	GCC	AGG	CCT	GTT	ATT	TTT	CCC	GAA	TCA	GAA	GCT	ACA	GAT	CAG	AAT	CAG	AAA	ACA	2553	
785	S	M	A	R	P	V	I	F	P	E	S	E	A	T	D	Q	N	Q	K	T	804	
2554	AAA	GGG	CCA	ATA	CTT	AAA	ATC	CAA	GGA	CTA	TGG	CAT	CCA	TTT	GCA	GTT	GCA	GCC	GAT	GGT	2613	
805	K	G	P	I	L	K	I	Q	G	L	W	H	P	F	A	V	A	A	D	G	824	
2614	CAA	TTG	CCT	GTT	CCG	AAT	GAT	ATA	CTC	CTT	GGC	GAG	GCT	AGA	AGA	AGC	AGT	GGC	AGC	ATT	2673	
825	Q	L	P	V	P	N	D	I	L	L	G	E	A	R	S	S	S	G	S	I	844	
2674	CAT	CCT	CGG	TCA	TTG	TTA	CTG	ACG	GGA	CCA	AAC	ATG	GGC	GGA	AAA	TCA	ACT	CTT	CTT	CGT	2733	
845	H	P	R	S	L	L	L	T	G	P	N	M	G	G	K	S	T	L	L	R	864	

Figure 9 (Continued)

SEQUENCE

2734	GCA ACA TGT CTG GCC GTT ATC TTT GCC CAA CTT GGC TGC TAC GTG CCG TGT GAG TCT TGC	2793
865	A T C L A V I F A Q L G C Y V P C E S C	884
2794	GAA ATC TCC CTC GTG GAT ACT ATC TTC ACA AGG CTT GGC GCA TCT GAT AGA ATC ATG ACA	2853
885	E I S L V D T I F T R L G A S D R I M T	904
2854	GGA GAG AGT ACC TTT TTG GTA GAA TGC ACT GAG ACA GCG TCA GTT CTT CAG AAT GCA ACT	2913
905	G E S T F L V E C T E T A S V L Q N A T	924
2914	CAG GAT TCA CTA GTA ATC CTT GAC GAA CTG GGC AGA GGA ACT AGT ACT TTC GAT GGA TAC	2973
925	Q D S L V I L D E L G R G T S T F D G Y	944
2974	GCC ATT GCA TAC TCG GTT TTT CGT CAC CTG GTA GAG AAA GTT CAA TGT CGG ATG CTC TTT	3033
945	A I A Y S V F R H L V E K V Q C R M L F	964
3034	GCA ACA CAT TAC CAC CCT CTC ACC AAG GAA TTC GCG TCT CAC CCA CGT GTC ACC TCG AAA	3093
965	A T H Y H P L T K E F A S H P R V T S K	984
3094	CAC ATG GCT TGC GCA TTC AAA TCA AGA TCT GAT TAT CAA CCA CGT GGT TGT GAT CAA GAC	3153
985	H M A C A F K S R S D Y Q P R G C D Q D	1004
3154	CTA GTG TTC TTG TAC CGT TTA ACC GAG GGA GCT TGT CCT GAG AGC TAC GGA CTT CAA GTG	3213
1005	L V F L Y R L T E G A C P E S Y G L Q V	1024
3214	GCA CTC ATG GCT GGA ATA CCA AAC CAA GTG GTT GAA ACA GCA TCA GGT GCT CAA GCC	3273
1025	A L M A G I P N Q V V E T A S G A A Q A	1044
3274	ATG AAG AGA TCA ATT GGG GGA AAC TTC AAG TCA AGT CAG CTA AGA TCT GAG TTC TCA AGT	3333
1045	M K R S I G E N F K S S E L R S E F S S	1064
3334	CTG CAT GAA GAC TGG CTC AAG TCA TTG GTG GGT ATT TCT CGA GTC GCC CAC AAC AAT GCC	3393
1065	L H E D W L K S L V G I S R V A H N A	1084
3394	CCC ATT GGC GAA GAT GAC TAC GAC ACT TTG TTT TGC TTA TGG CAT GAG ATC AAA TCC TCT	3453
1085	P I G E D D Y D T L F C L W H E I K S S	1104
3454	TAC TGT GTT CCC AAA TAA ATG GCT ATG ACA TAA CACTATCTGAAGCTCGTTAAGTCTTTTGCCCTCTCT	3521
1105	Y C V P K * M A M T *	5
3522	G ATG TTT ATT CCT CTT AAA AAA TGC TTA TAT ATC AAA AAA TTG TTT CCT CGA TTA AAA	3579
1	M F I P L K K C L Y I K K L F P R L K	19
3580	AAA AAA AAA AAA AAA AAA AAA AAA	3606
20	K K K K K K K K K K	28

Figure 9 (Continued)

Figure 10

[illegible]

0529239.10200

TTTTTTGGTTGCTAACAAATAAAGGTATACGGTTTTATGTCATCAATATAA	50
CTATATATAAAAGAAATGAAAGATATATATTGTTTTTTCATTTATCAAAC	100
AAAACAACAAGACTTTTTTTTTTACTTTTTTACATTGGTCAACAAAATACAA	150
GATAAACGACATCGTTTAATCATTTCCTCAATTTTACCCCTAAGTTTAACA	200
CCTAGAACCTTCTCCATCTTCGCAAGCACAGCCTGATTAGGAACAGCTTT	250
ACCATTCTCATATTCTGAACTACCTGAGTCCTCTCATTGATCTGTTTCG	300
CCAAATCCGCTTGTGACATCTTCTTCTCCAATCTCGCTTTCTGTATCATC	350
AACCTCACCTCTGCTTTCACACGATCCATCGCCGAGGCTCTGTTTCTTC	400
TTCCAGCTTCTTCGTGTTAATCACCGGAACCGCCGTAGATTTCCCTTTT	450
TGTTTGAACCGGCATCGAATTTCTTAACCGTTTGAACCGCGACACCGTTT	500
CTCAGAGCTGCGTTAACCGCTTTCGGATCGCGTAGGTCTTGCTCTTTTG	550
TTTTGATTGTGGAGAACTACTGGTTCCCAGTCTTGTTACTGCTCCTG	600
GGTATCTGCTCGGCATCGTCGATGAATTGAGAGAAAGGAACAACGCGAAA	650
ATTTTATTAATCTGAGTTTTGAAATTGAGAAACGATGAAGATGAAGAATG	700
TTGTTGAGAGGATTGTGATATTTATATATACGAAGATTGGTTTCTGGAGA	750
ATTGATCATCTTTTTCTCCATTTTCGTCTCTGGAACGTTCTTAGAGATG	800
ATTGACGACGTGTCAATTATCTGATTTGCAGTTAACCAATGCTTTTTGGGT	850
TGGATTCTGTGGTACACCATATTATCCGATTTGGCTCAATGGTTTTATATA	900
AATTTGGTTTTTCGGTTTCGGTTATGAGTTATCATTTAAATTAAGCTAACCA	950
AAAATTTTCGTAAAATTTATTTTCGGTTTCAATTCGGATCCCTTACTTCCA	1000
GAACCGAATTATTCGAACCGGGGTTAGCCGAACCGAATACCAATGCCTG	1050
ATTGACTCGTTGGCTAGAAAGATCCAACGGTATACAATAATAGAACATAA	1100
ATCGGACGGTCATCAAAGCCTCAAAGAGTGAACAGTCAACAAAAAAGTT	1150
GAGCCCTGAGGAGTATCGTTTCCGCCATTTCTACGACGCAAGGCGAAAAAT	1200
TTTTGGCGCCAATCTTTCCCCCTTTTCAATTCTCTCAGCTCAAAACATC	1250
GTTTCTCTCTCACTCTCTCTCACAATTCCAAAAAATGCAGCGCCAGAGAT	1300
CGATTTTGTCTTTCTTCCAAAAACCCACGGCGGCGACTACGAAGGGTTTG	1350
GTTTCCGGCGATGCTGCTAGCGCGGGGGCGGCAGCGGAGACCACGATTT	1400
AATGTGAAGGAAGGGGATGCTAAAGGCGACGCTTCTGTACGTTTTGCTGT	1450
TTCGAAATCTGTGATGAGGTTAGAGGAACGGATACTCCACCGGAGAAGG	1500
TTCCGCGTCGTGTCCTGCCGTCTGGATTTAAGCCGGCTGAATCCGCCGGT	1550
GATGCTTCGTCCCTGTTCTCCAATATTATGCATAAGTTTGTAAAAGTCGA	1600
TGATCGAGATTGTTCTGGAGAGAGGTACTAATCTTCGATTCTCTTAATTT	1650
TGTTATCTTTAGCTGGAAGAAGAAGATTCTGTGAATTTGTTGTATTCTGTT	1700
GGAGAGATTCTGATTACTGCATTGGATCGTTGTTTACAAATTTTCAGGAG	1750
CCGAGAAGATGTTGTTCCGCTGAATGATTCTCTATGTATGAAGGCTA	1800
ATGATGTTATTCTCAATTTTCGTTCCAATAATGGTAAACTCAAGAAAGA	1850
AACCATGCTTTTAGTTTTCAGTGGGAGAGCTGAACTTAGATCAGTAGAAGA	1900
TATAGGAGTAGATGGCGATGTTCCCTGGTCCAGAAACACCAGGGATGCGTC	1950
CACGTGCTTCTCGCTTGAAGCGAGTTCTGGAGGATGAAATGACTTTTAAG	2000
GAGGATAAGGTTCTGTATTGGACTCTAACAAAAGGCTGAAAATGCTCCA	2050
GGATCCGGTTTGTGGAGAGAAGAAAGAAGTAAACGAAGGAACCAAATTTG	2100
AATGGCTTGAGTCTTCTCGAATCAGGGATGCCAATAGAAGACGTCCTGAT	2150
GATCCCTTTACGATAGAAAGACCTTACACATACCACCTGATGTTTTCAA	2200

Figure 11

0529239.102700

GAAAATGTCTGCATCACAAAAGCAATATTGGAGTGTTAAGAGTGAATATA	2250
TGGACATTGTGCTTTTCTTTAAAGTGGTTAGTAACTATTAATCTAGTGTT	2300
CAATCCATTTCTCAATGTGATTTGTTCACTTACATCTGTTTACGTTATG	2350
CTCTTCTCAGGGGAAATTTTATGAGCTGTATGAGCTAGATGCGGAATTAG	2400
GTCACAAGGAGCTTGACTGGAAGATGACCATGAGTGGTGTGGGAAATGC	2450
AGACAGGTAAATTAGTTGAAACAACCTGGCCTGCTTGAATTATTGTGTCTA	2500
TAAATTTTGACACCACCTTTTGTTCAGGTTGGTATCTCTGAAAGTGGGA	2550
TAGATGAGGCAGTGCAAAAGCTATTAGCTCGTGGGTAAGGGAACCATCAT	2600
ACTTTATGGAATTCGTTTACTGCTACTTCGGCTAGGATTTAAGAAATGGA	2650
AATCACTTCAAGCATCATTAGTTAGGATCCTGAGAACTCAGGATGTTTTCT	2700
TTATTCGTTATATAATAAGTCTTTTCATCAAGGAGTAACAAACAAAACCTT	2750
GCACAATATTTGTGTGCTCACTGGCAAGGCATATATACCCAGCTAACCTT	2800
TGCTAGTTCACTGTAGTAACAGTTACGGATAATATATGTTTACTTGTATG	2850
TGGTACCCCTCATTTTGTCTCTCATGGAGGCTTTEAAGCCTTGTGTTGAAA	2900
CTGGATAGTTACATATGCTTCCAACAGAACTAGCATGCAGATTCATATG	2950
CTTTCCTATTCTACTAATTATGTATTGACACACTCGTTGTTTCTTTTGAA	3000
AGATATAAAGTTGGACGAATCGAGCAGCTAGAAACATCTGACCAAGCAAA	3050
AGCCAGAGGTGCTAATACTGTAAGTTTTCTTGGATAGGTCAAGGAGAGTG	3100
TTGCAGACTGTTTTGATCATTTCTTTTCTGTACATTACTTTCATGCTG	3150
TAATTAACCTCAATGGCTATTCTGGTCTGATTATCAGATAATTCCAAGGAA	3200
GCTAGTTCAGGTATTAACCTCCATCAACAGCAAGCGAGGCAACATCGGGC	3250
CTGATGCCGTCCATCTTCTTGCTATAAAAGAGGTTTGTATTACTTATT	3300
TATCTTATCATGTTTCAGTTCATCCAAGTCCTGAAAAATTACACTCTTCTT	3350
TACCAATCTTCCATCAAGCTGTGTAAAGGATTTGGAATTAGAAAAATCATT	3400
ATTTGATGCTTTGTTTTATATGCAAGAGGTTCCCTTGAAAAGATCTGTTT	3450
AAGATTCTTTGCACCTGAAAAATTCAATCTTTTTAAGTGAATCCCTACT	3500
TTCTTACAATGATCATAGTCTGCAATTGCATGTCAAGTAATATCATTCCT	3550
TGTTACTGCATCCCCCTCTTTCTTAATGACCATTGTCTATGTTGTGTTTG	3600
TCTCGTGTGCTGGAGAAAATGATAGCTGATCCAAGCTGTACATTATCATG	3650
ATTAAGTAGCTGCTCAGGAATTGCCTTTGGTTACATTGCCTAATGGTTTG	3700
ATGTCAATTTTTCTTCTGAATCTTTATTTTAGATCAAAATGGAGCTACAA	3750
AAGTGTTCAACTGTGTATGGATTTGCTTTTGTGACTGTGCTGCCTTGAG	3800
GTTTTGGGTTGGGTCCATCAGCGATGATGCATCATGTGCTGCTCTTGGAG	3850
CGTTATTGATGCAGGTAAGCAAGTGATTCTGTATCTTATGTGTACCATG	3900
TGACTTCCTGTGCATATATTTGGGTTGCAGGAACATAATTCTGAATCACCA	3950
TTTGGTATGTTTTTCCAGGTTTCTCCAAAGGAAGTGTTATATGACAGTA	4000
AAGGTAAACTGCTTGTATCGCCAGTTGTTTTGTTAAACAGAATTTAAGGT	4050
AAATGACACTGGTTAATTTAAAGTGCATACATGTTGAAATATTGCAGGGC	4100
TATCAAGAGAAGCACAAAAGGCTCTAAGGAAATATACGTTGACAGGTACC	4150
ATTTCAAGTAGGCAAGCTAACTGACAATTTAACCGCTCACCGAATGATAGG	4200
TCTCTTAAACATTGCTAATGTAGATGATGTTTATGTTTCAATCTAATAGG	4250
GTCTACGGCGGTACAGTTGGCTCCAGTACCACAAGTAATGGGGGATACAG	4300
ATGCTGCTGGAGTTAGAAATATAATAGAATCTAACGGATACTTTAAAGGT	4350
TCTTCTGAATCATGGAACGTGTGCTGTTGATGGTCTAAATGAATGTGATGT	4400

Figure 11 (Continued)

TGCCCTTAGTGCTCTTGGAGAGCTAATTAATCATCTGTCTAGGCTAAAGG 4450
 TGTGTTGGCTTGTGTTAGTTTTGCTTTTCACAAATTAAGCAAAGGAACTT 4500
 TTCATAACTTACAGTTTCTATCTACTTGCAGCTAGAAGATGTACTTAAGC 4550
 ATGGGGATATTTTTCCATACCAAGTTTACAGGGGTGTCTCAGAATTGAT 4600
 GGCCAGACGATGGTAAATCTTGAGATATTTAACAATAGCTGTGATGGTGG 4650
 TCCTTCAGGCAAGTGCATATTTCTTTTTTGATAACTTCAACTAGAGGGCA 4700
 GACATAGAAGGAAAAATTCTAATACTTCGTACGGATCTCCAGTAAGTAAT 4750
 AGCCGATTTTTGTTTACCTATGTAGGGACCTTGTACAAATATCTTGATAA 4800
 CTGTGTTAGTCCAACCTGGTAAGCGACTCTTAAGGAATTGGATCTGCCATC 4850
 CACTCAAAGATGTAGAAAGCATCAATAAACGGCTTGATGTAGTTGAAGAA 4900
 TTCACGGCAAACCTCAGAAAGTATGCAAATCACTGGCCAGTATCTCCACAA 4950
 ACTTCCAGACTTAGAAAGACTGCTCGGACGCATCAAGTCTAGCGTTCGAT 5000
 CATCAGCCTCTGTGTTGCCTGCTCTTCTGGGGAAAAAGTGCTGAAACAA 5050
 CGAGTAAGTATCAATCACAAGTTTTCTGAGTAATGCCTTCCATGAGTAGT 5100
 ATAGGACTAAACATTACGGGTCTAGCTAAAGACTGTTCTCTCTCTTTTG 5150
 CAATGTCTGGTTATTACCTACATTTCTCTTAACCTATTGCAATTCAGGTT 5200
 AAAGCATTTGGGCAAATTGTGAAAGGGTTCAGAAGTGAATTGATCTGTT 5250
 GTTGGCTCTACAGAAGGAATCAAATATGATGAGTTTGCTTTATAAAGTCT 5300
 GTAAACTTCCTATATTAGTAGGAAAAAGCGGGCTAGAGTTATTTCTTTCT 5350
 CAATTGGAAGCAGCCATAGATAGCGACTTTCCAAATTATCAGGTGCCCAT 5400
 CTATCTTTCATACTTTACAACAAAATGTCTGTCACTACTCAAAGCAATGC 5450
 ATATGGCTTAGATCTCAACTCACACCCCGAGGATCCTAAAGGGATTGCT 5500
 TTTTATTCTTAATGTTTTGGATGGTTTGATTTATTTCTAACTTGAAGT 5550
 ATTAATCTTGTACCAGAACCAAGATGTGACAGATGAAAACGCTGAAACTC 5600
 TCACAATACTTATCGAAGTTTTATCGAAAGAGCAACTCAATGGTCTGAG 5650
 GTCATTACACCATAAGCTGCCTAGATGTCTGAGATCTTTTGCAATCGC 5700
 AGCAAGTCTCTCTGCTGGAAGCATGGCCAGGCCTGTTATTTTTCCGGAAT 5750
 CAGAAGCTACAGATCAGAATCAGAAAACAAAAGGGCCAATACTTAAAATC 5800
 CAAGGACTATGGCATCCATTTGCAGTTGCAGCCGATGGTCAATTGCCTGT 5850
 TCCGAATGATATACTCCTTGGCGAGGCTAGAAGAAGCAGTGGCAGCATTC 5900
 ATCCTCGGTCAATTGTTACTGACGGGACCAACATGGGCGGAAAATCAACT 5950
 CTTCTTCGTGCAACATGTCTGGCCGTTATCTTTGCCCAAGTTTGTATACT 6000
 CGTTAGATAATTACTCTATTCTTTGCAATCAGTTCTTCAACATGAATAAT 6050
 AAATTCTGTTTTCTGTCTGCAGCTTGGCTGCTACGTGCCGTGTGAGTCTT 6100
 GCGAAATCTCCCTCGTGGATACTATCTTCACAAGGCTTGGCGCATCTGAT 6150
 AGAATCATGACAGGAGAGAGTAAGTTTTGTTCTCAAATACCAATTCCTC 6200
 GAACTATTTACTCAGATTTTGTCTGATTGGACAAGGTGGTTTTGCTTTTT 6250
 TTTAGGTACCTTTTTGGTAGAATGCACTGAGACAGCGTCAGTTCTTCAGA 6300
 ATGCAACTCAGGATTCAGTAGTAATCCTTGACGAACTGGGCAGAGGAACT 6350
 AGTACTTTTCGATGGATACGCCATTGCATACTCGGTAACCTGCTCTTCTCC 6400
 TTCAACTTATACTTGTGATCAACAAAAACATGCAATTCAATTTGCTGAA 6450
 ACTTATTGATTTATATCAGGTTTTTCGTACCTGGTAGAGAAAGTTCAAT 6500
 GTCGGATGCTCTTTGCAACACATTACCACCCTCTCACCAGGAATTGCGG 6550
 TCTCACCACGTTGTCACCTCGAAACACATGGCTTGCGCATTCAAATCAAG 6600

Figure 11 (Continued)

ATCTGATTATCAACCACGTGGTTGTGATCAAGACCTAGTGTCTTGTACC 6650
GTTTAACCGAGGGAGCTTGTCTGAGAGCTACGGACTTCAAGTGGCACTC 6700
ATGGCTGGAATACCAAACCAAGTGGTTGAAACAGCATCAGGTGCTGCTCA 6750
AGCCATGAAGAGATCAATTGGGGAAAACCTCAAGTCAAGTGAGCTAAGAT 6800
CTGAGTTCTCAAGTCTGCATGAAGACTGGCTCAAGTCATTGGTGGGTATT 6850
TCTCGAGTCGCCCACAACAATGCCCCCATTTGGCGAAGATGACTACGACAC 6900
TTTGTTTTGCTTATGGCATGAGATCAAATCCTCTTACTGTGTTCCTAAAT 6950
AAATGGCTATGACATAACACTATCTGAAGCTCGTTAAGTCTTTTGCTTCT 7000
CTGATGTTTATTCTCTTAAAAAATGCTTATATATCAAAAAATTGTTTCC 7050
TCGATTATAACAAGATTATATATGTATCTGTGCGTTTAGCTATGGTATAT 7100
AATATATGTATGTTTCATGAGATTGGTCAAGAGAAATACTCACAAACAGTA 7150
TATTAAGAAGGAAATATGTTTATGCATTAATTTAAGTTTCAAGATAAACT 7200
GCAAATAACCTCGACTAAAGTTGCAAAGACCAAACACAAATTACAAAAC 7250
TATAAGACTTAAGTTCTGAATTCCTTAAACCAAAAAAAAAAACAGAAC 7300
TATTTTGTTGCATCTACAAACAACACAAACCTACATAGTTTATAACTTAC 7350
TCATCACTGAGATTAACATCAGAATCATTCTCCATTTCTTCATCTTCACT 7400
CTCATCATCATCACCACCACCATGATGATTCTCCTCCTCTTCACGTAACC 7450
TAGCAATCTCACTCTGAGCTCTATCAACAATCTGCTTCTTCTGCAACTCC 7500
AAATCTCTCTGAAAATCAGCTCTCATCTTCTCCAACCTCCTTCATTTGCTC 7550
TTTCTTACTCTTCTCCATCTTCTCATAAACCTTCCCAAACCTCTCAACAG 7600
AATCCGCCAACATCTTATACGAAGCAGCGTCATTAACCTTCTTCCTCTCG 7650
TACTCAACCTCATCATCCTCATCCTCCTCCTCTTCAGAATCACCAGGACT 7700
ATCCATCATCTCATCAAACCCATTAGACTTATCTAAATAAACCTTAGTGT 7750
TCATAAACACAAACTCACCTGAATCAACACCACAAGCTAAACCTAAATCC 7800
GACTTGGGCGAAACACAAAGCAACATATCCAACCTTATTGAAAAACGACCA 7850
TTTACTTGAACCTAAACCTGATTTCTCAACCTTAATCTTCTCTTTTCTAT 7900
ACTTCCTCTTCAAGTCATCAATCATCTCTCCTACATTGCGTCTCAGATTC 7950
TCCATCCTTAGCTCCTCACTCACTTCTCAGCTACTTCATTCCAATCCTC 8000
GTTCTCAAACTCCTTCTACCCAATTGCAAAAACCTATCTCCCCAACTT 8050
CAAGCAACACAA 8062

Figure 11 (Continued)

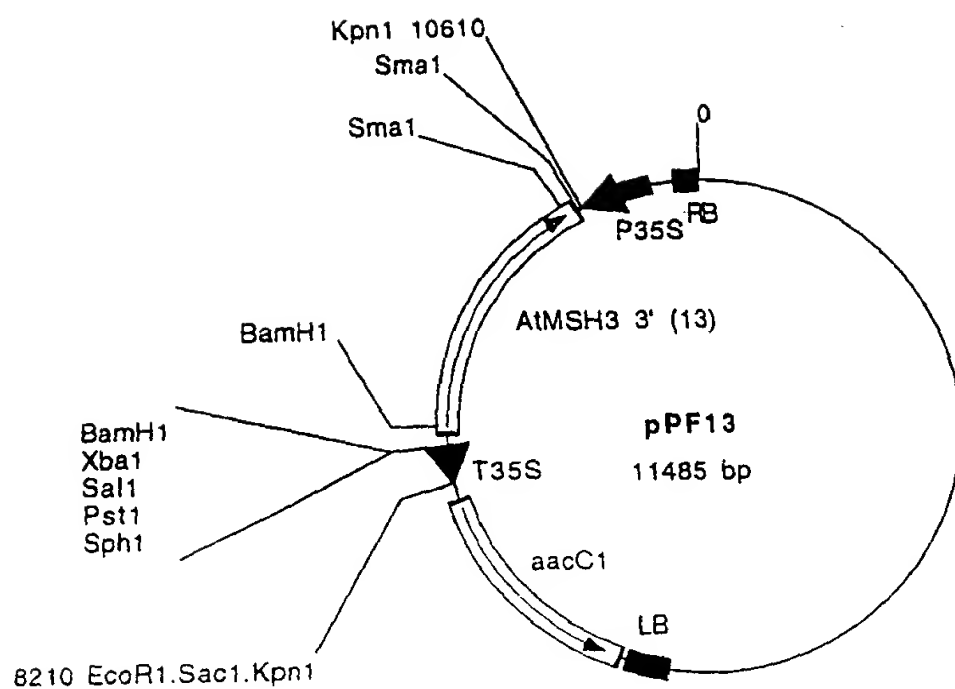


Figure 12

Comments/References: AtMSH3 3' side antisense : AtMSH3 3' (13 = 2104bp) from pUC18/13 Sal1/Sst1/T4 into pCW164 BamH1/T4 in Agrobacterium LBA4404

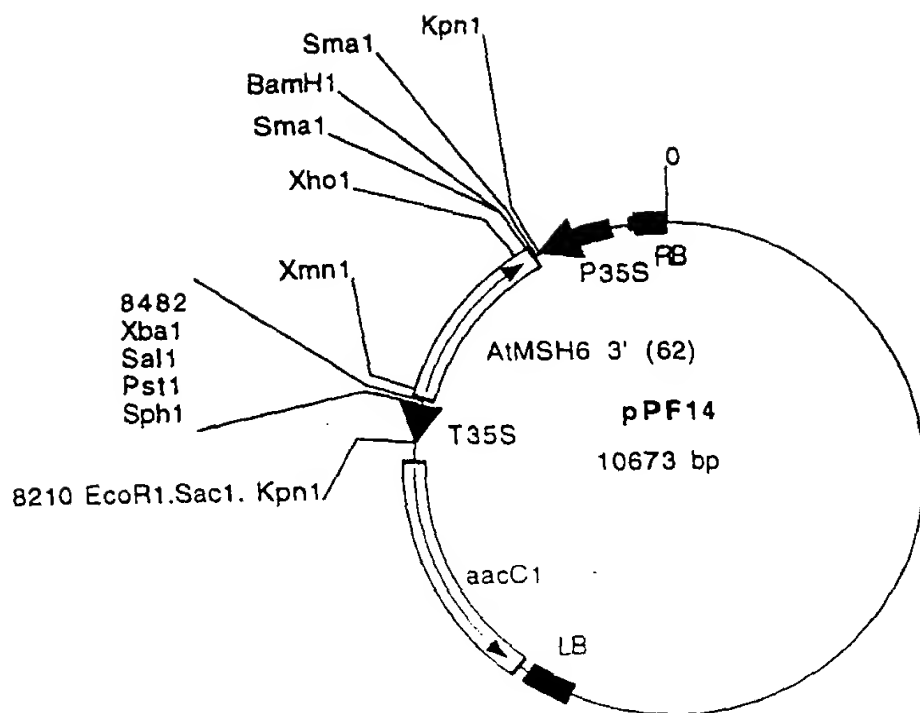


Figure 13

Comments/References: AtMSH6 (S8) 3' side antisens : 62 Sal1/Sst1/T4 (1379bp)
into pCW164 BamH1/T4

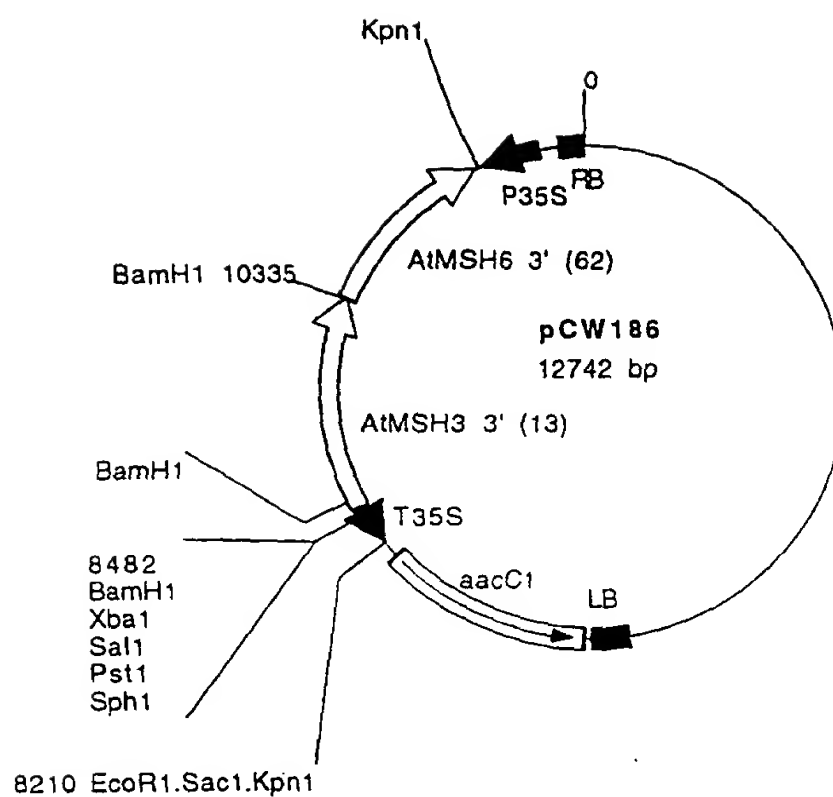


Figure 14

Comments/References: AtMSH6 3'/AtMSH3 3' antisense : AtMSH6 (S8) 3' side (62=1379bp)
 Sal1/Sst1/T4 into pPF13 (pCW164 AtMSH3 (S5) 3' side (13=2104) antisense)/Sma1. in
 LBA4404

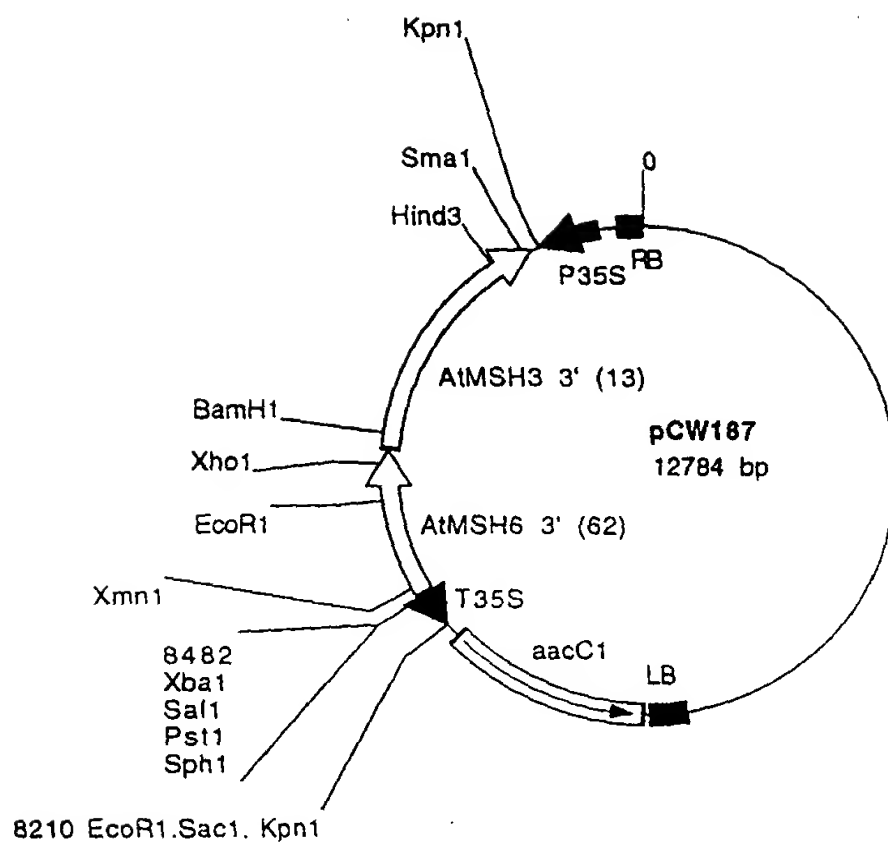


Figure 15

Comments/References: AtMSH3 3'/AtMSH6 3' antisens (D) : AtMSH3 (S5) 3' side (13=2104bp) Sal1/Sst1/T4 into pPF14 (AtMSH6 (S8) 3'side (62=1379bp) antisense into pCW164)/Sma1. in LBA4404

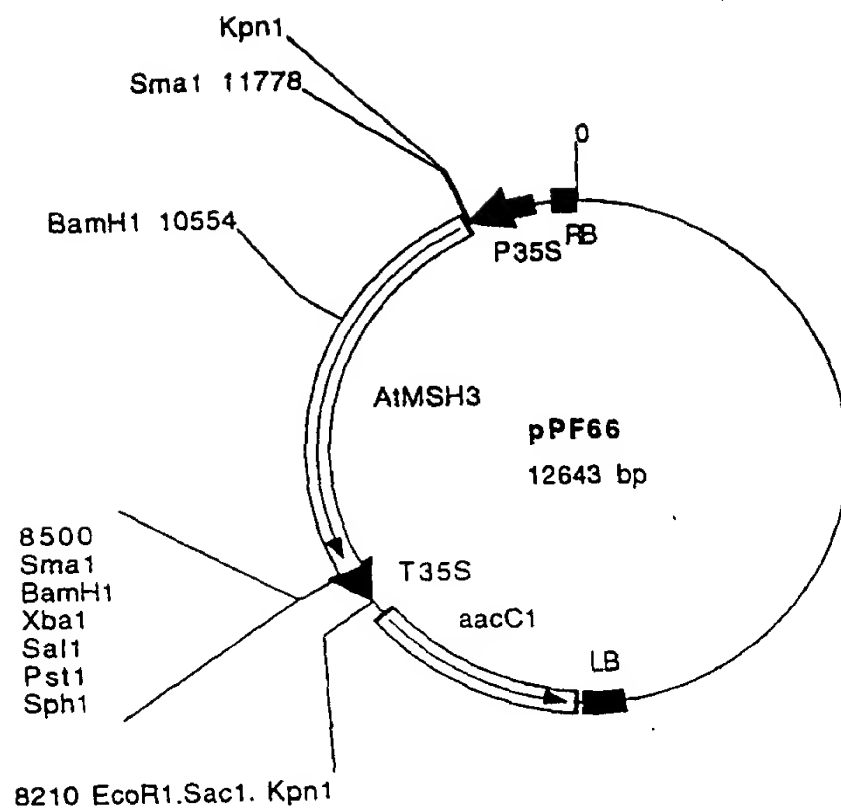


Figure 16

Comments/References: AIMS H3 (S8) complete, sense orientation : pPF26 (3342bp)
Sma1 into pCW164 Sma1

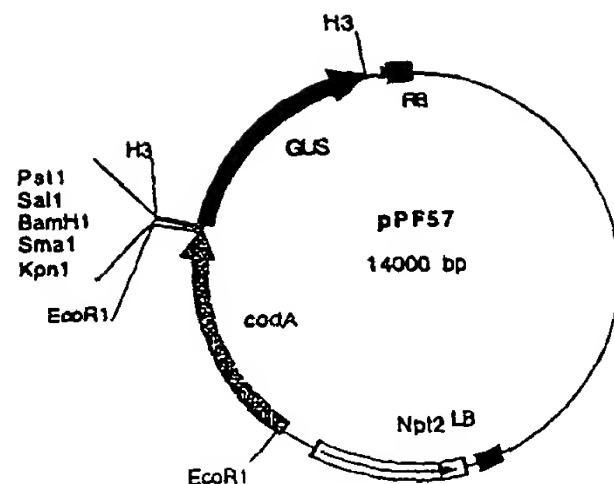


Figure 17

Comments/References: pPZP111 with *codA* *EcoR1* cassette in *EcoR1* site and *Hind3* GUS cassette in *Hind3* site. KanR. All genes under Promoter/terminator 35S

Figure 18

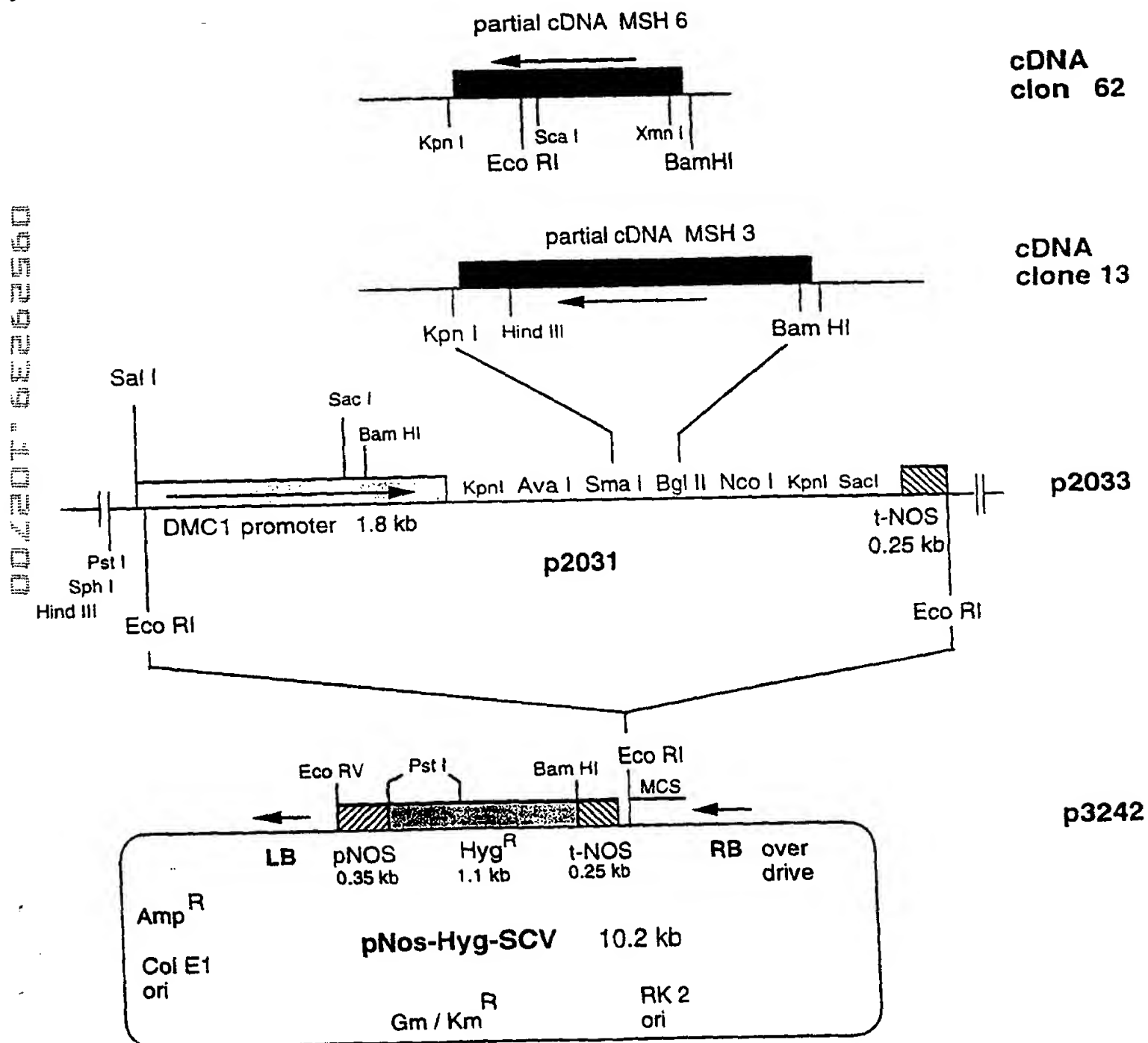


Figure 19

p3243

